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Technical note

Automated bone landmarks prediction on the femur using anatomical deformation technique

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ABSTRACT

Anatomical landmarks on bones play important roles in musculoskeletal simulations and surgical planning. This study develops an anatomically deformable model of the femur to predict bone landmarks automatically and quantifies its prediction accuracy. Forty-three angiographic computed tomography (CT) images of femurs were collected and 14 bone landmarks were manually marked on these images by experts. Surface mesh models of the femur were extracted from the CT images and combined with the bone landmark information to create an anatomical deformable model. The anatomical deformation technique developed in this study predicted bone landmarks automatically as the surface of a deformable model was matched to the surface of a given femur model. The prediction accuracy was quantified using the leave-one-out cross-validation method. The average prediction error for the 14 landmarks ranged from 2.80 to 5.93 mm. While the prediction accuracies of anterior and posterior cruciate ligaments and lateral epicondyle sites were high with averages (standard deviation) of 3.00 (±1.55), 2.80 (±1.76) and 2.97 (±1.87) mm, respectively, those of gluteus minimus, ligament of head of femur and piriformis sites were low with averages of 5.93 (±3.77), 4.89 (±3.49) and 4.87 (±2.70) mm, respectively. Accuracy can be expected to increase with the use of more population data as is the nature of a population-based statistical deformable model.

1. Introduction

Anatomical landmarks on the bone surface play very important roles in determining the surgical reference points for total joint replacements and biomechanical applications. In navigation surgery techniques bone landmarks are marked using a probe with optical ball markers to obtain 3-dimensional (3D) positions. Based on the bone landmark positions surgical guides and cutting tools are aligned with the bone and joint [1]. Biomechanical human musculoskeletal simulation requires a skeletal model with muscles attached. The muscle attachment locations that can be obtained from bone landmarks determine the length of muscle moment arm and significantly affect the accuracy of simulation results [2].

Previous studies reported that the visual marking of the bone landmarks on denuded cadaveric bones during a simulated and navigation based total knee surgery had relatively large errors in both intra-observer and inter-observer repeatability [3–5]. The mean errors for 6 anatomical points around the knee ranged from 4.9 to 11.1 mm and statistically significant differences existed between observers in identifying most of the anatomical points [5]. On the other hand, the identification of bone landmarks on the femur and tibia in 3D anatomical images from computed tomography (CT) had relatively high intra-observer and inter-observer reproducibility. When tested with 3 observers on 17 bone landmarks on the femur and tibia, the mean intra-observer error ranged from 0.4 to 1.4 mm and the mean inter-observer error ranged from 0.3 to 3.5 mm [6].

Automated bone landmark prediction has been introduced in previous studies. Beil et al. could detect bone landmarks based on the local curvature of isocontours in 3D images with information on the initial manual localization [7]. Automatic prediction of bone landmarks based on pure geometric analysis achieved high reproducibility but it could not be guaranteed that the anatomical landmarks were always on the geometrically distinctive points [7,8]. A 3D template matching technique to localize the bone landmarks on the knee was introduced [9] but the technique used the bone landmarks pre-determined from a single template model, which

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did not reflect the population variation of the bone landmark positions.

The statistical shape modeling technique to predict target model shape from the shapes of database models has achieved a great advancement for the last decade [10,11]. Previously, we have developed a human body shape modeling method that creates a statistical shape model with variations from a large number of human body shape population data [12] utilizing the principal component analysis (PCA) [13]. Related to the bone shapes, similar insights have been recently applied to the human femur for the purpose of obtaining a statistically-based finite element (FE) model of the bone [14–16]. This type of statistical approach utilizes the population shape database and predicts a target shape within the variations that exist in the population.

In this study, we developed a novel statistical bone landmarks prediction method by utilizing the statistical shape modeling and shape prediction methods. The base data set contained not only the coordinates of points that compose model shapes but also the coordinates of points for bone landmarks. In the pre-process of creating a consistent mesh for each of the base data, the bone landmarks were assigned the consistent index throughout all base data. Assuming that the 3D bone surface shape of a new subject could be relatively easily obtained from 3D imaging data such as CT [17,18] or from a reconstruction of two-dimensional images [19], our statistical shape model calculated from the consistent mesh models could predict the bone landmarks on this surface model statistically based on the population data.

The suggested algorithm was tested with 43 human femur models with bone landmarks marked by clinical experts. The performance of the bone landmarks prediction was measured using the leave-one-out cross-validation method. The accuracy for the prediction of bone landmarks against the landmarks marked manually by clinical experts was quantified.

2. Methods

2.1. Data acquisition

An internal review board (IRB) approval was obtained from the Chung-Ang University Hospital before the study. Forty-three angiographic CT images without patients identification were obtained from the database of the Department of Radiology. Fourteen anatomical landmarks on the femur were selected for this study, which are frequently used in navigation surgery of the knee [6] and in biomechanical musculoskeletal simulation [20,21]. The target bone landmarks are listed in Table 1. Two landmarks in the list were the bony eminences, 3 landmarks were the ligament attachment sites, and the rest were the insertion and origin sites of muscles. Some of the landmarks were frequently used to determine a joint's coordinate system [20,22]. The muscles in the list are the major muscles used during various activities; thus, their attachment locations are important for determining muscle activation level and internal muscle forces in musculoskeletal simulations [21].

An experienced musculoskeletal radiologist and an orthopedic surgeon identified 14 bone landmarks on the right femur in 43 angiographic CT images. The orthopedic surgeon had previously performed intensive dissections on the distal femur of a number of cadaveric knees to understand the attachment sites for ligaments and muscles as shown in Fig. 1.

The observers used the Osirix medical image viewer [23] to locate bone landmarks in the CT images as this shows very high accuracy and reproducibility [6]. The multi-planar reconstruction tool in Osirix visualizes CT data in any oblique plane aiding identification of the bone landmarks as in Fig. 2.

Table 1
List of selected anatomical landmarks on the femur.

No.	Name of landmark	Type
1	Obturator internus	Muscle insertion
2	Piriformis	Muscle insertion
3	Gluteus minimus	Muscle insertion
4	Psoas	Muscle insertion
5	Adductor magnus distal	Muscle insertion
6	Obturator externus superior	Muscle insertion
7	Gastrocnemius medialis	Muscle origin
8	Popliteus	Muscle origin
9	Gastrocnemius lateralis	Muscle origin
10	Ligament of head of femur	Ligament attachment
11	Anterior cruciate ligament (ACL)	Ligament attachment
12	Posterior cruciate ligament (PCL)	Ligament attachment
13	Medial epicondyle	Bony eminence
14	Lateral epicondyle	Bony eminence

2.2. Consistent mesh with bone landmarks

3D geometric models of the femur in the right leg were obtained from 43 CT scans using custom medical image segmentation software [18]. The accuracy of 3D models reconstructed using the software was previously reported [18]. The surface model of the femur consisted of triangular meshes and vertices. In mesh-based statistical shape processing, mesh models should have identical topology or connectivity between triangular meshes so that the compatibility between the models is guaranteed. However, the surface mesh topologies and number of vertices of bone models generated from CT data using surface reconstruction techniques differ from each other. Therefore, before performing the statistical shape analysis, the meshes of a bone model should be re-parameterized so that it has consistent and identical topology. For this reason, we employed a template-based mesh re-parametrization technique [12]. In this re-parametrization technique, template mesh was deformed to minimize shape disparity so that the resultant deformation had the same shape as the target model while the original mesh topology of the template remained intact. This technique was applied to every model in the database, to give a set of models with the shape of the original individual and the unique topology inherited from the template. Shape disparity was defined by an error functional, which includes 4 energy terms: disparity error, smoothness error, landmark error, and distortion error. Most importantly, the role of the landmark error was to guarantee that the bone landmarks in the template model were exactly matched to the corresponding bone landmarks in the target. By doing so, we could guarantee one-to-one correspondences between the anatomical landmarks, and therefore, the vertex indices of the landmarks were identical despite variations in bone shape.

2.3. Anatomical deformation of the bone shape with landmarks

With confirmed consistent topology between femur models, we defined a meaningful mathematical quantity representing the shape of a bone; the shape vector was defined as an array of coordinate values of a consistent mesh model and represented the shape of the corresponding bone model:

$$\mathbf{x} = [x_1, y_1, z_1, x_2, y_2, z_2, \dots, x_n, y_n, z_n]^T.$$

The shape vectors of each model were collected to build a data matrix $\mathbf{X} = [\mathbf{x_1}, \dots, \mathbf{x_m}]$ where m was the number of models in the database. By using a matrix decomposition technique, one can decompose the column space of the matrix $\mathbf{X}$ into 2 separate subspaces, one of which is possibly a meaningful subspace and the other is noise. In our study, we employed the PCA as the matrix decomposition technique to obtain m principal component vectors that span the column space of the matrix $\mathbf{X}$ in order of importance.